

**AMENDMENT**

**In the Specification:**

Please amend the paragraph beginning at page 32, line 7 as follows:

Additional HCV epitopes for use in the MEFAs include any of the various epitopes described above, such as epitopes derived from the hypervariable region of E2, such as a region spanning amino acids 384-410 or 390-410, or the consensus sequence from this region[.] as described above (Gly-Ser-Ala-Ala-Arg-Thr-Thr-Ser-Gly-Phe-Val-Ser-Leu-Phe-Ala-Pro-Gly-Ala-Lys-Gln-Asn) (SEQ ID NO: 7), which represents a consensus sequence for amino acids 390-410 of the HCV type 1 genome. A representative E2 epitope present in a MEFA of the invention can comprise a hybrid epitope spanning amino acids 390-444. Such a hybrid E2 epitope can include a consensus sequence representing amino acids 390-410 fused to the native amino acid sequence for amino acids 411-444 of HCV E2.